Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:01:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716293.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR9716293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716293.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:01:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,586,734
Mapped reads	2,411,558 / 93.23%
Unmapped reads	175,176 / 6.77%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	47,790 / 1.85%
Read min/max/mean length	30 / 101 / 101.67
Duplicated reads (estimated)	158,485 / 6.13%
Duplication rate	5.07%
Clipped reads	2,454,976 / 94.91%

2.2. ACGT Content

Number/percentage of A's	46,840,509 / 25.07%
Number/percentage of C's	39,061,969 / 20.9%
Number/percentage of T's	55,260,926 / 29.57%
Number/percentage of G's	45,702,083 / 24.46%
Number/percentage of N's	8,081 / 0%
GC Percentage	45.36%

2.3. Coverage

Mean	0.0604

Standard Deviation	0.4822

2.4. Mapping Quality

Mean Mapping Quality	46.48

2.5. Mismatches and indels

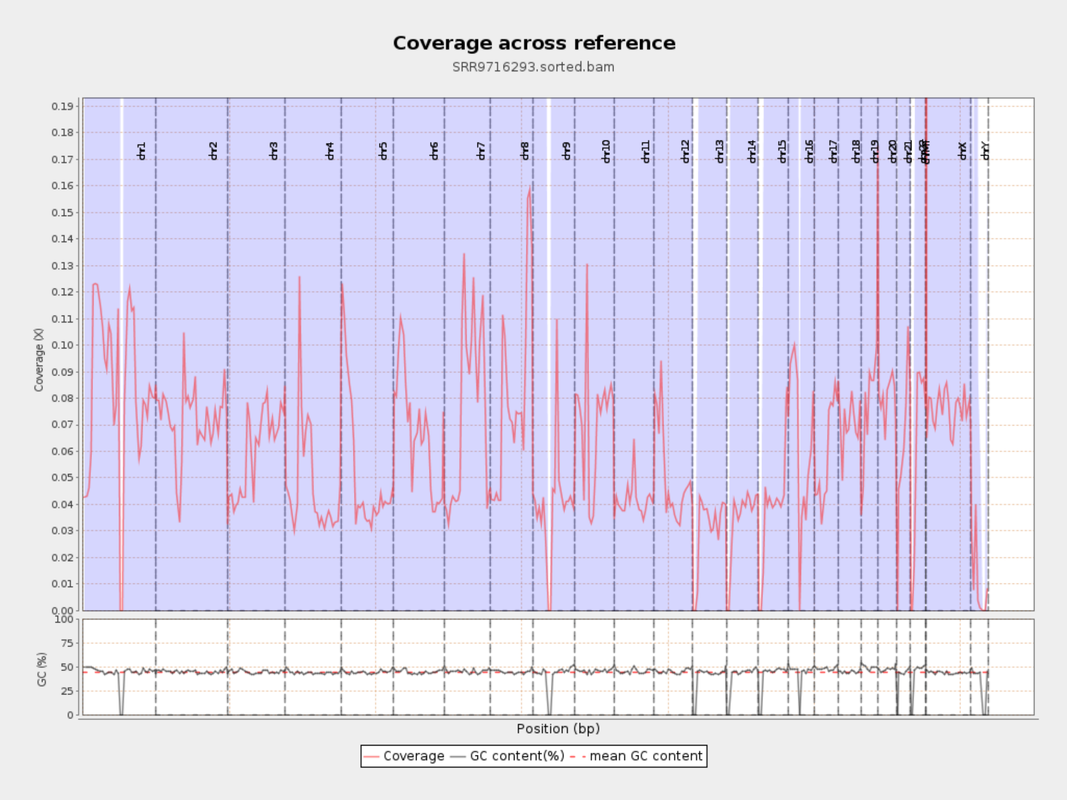
General error rate	0.68%
Mismatches	1,237,909
Insertions	15,629
Mapped reads with at least one insertion	0.64%
Deletions	34,171
Mapped reads with at least one deletion	1.39%
Homopolymer indels	39%

2.6. Chromosome stats

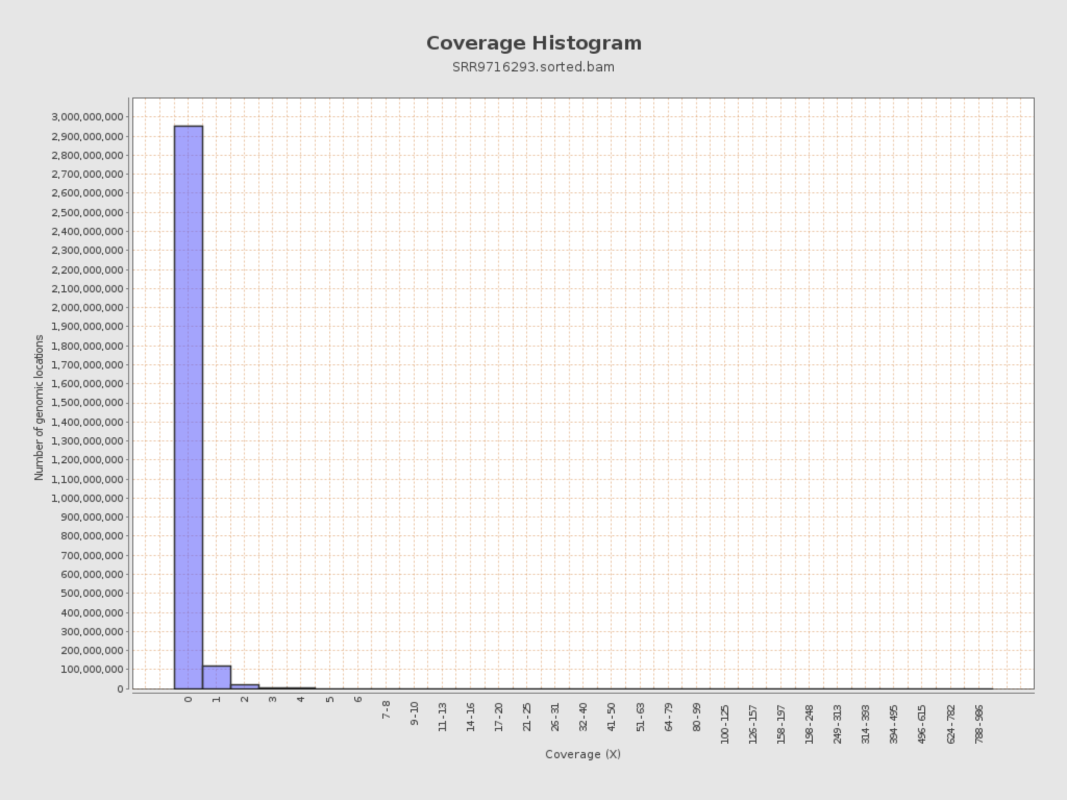
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20692865	0.083	0.914
chr2	243199373	17554090	0.0722	0.5192
chr3	198022430	11932168	0.0603	0.3061
chr4	191154276	9028531	0.0472	0.4165
chr5	180915260	9508214	0.0526	0.2882
chr6	171115067	11436231	0.0668	0.3426
chr7	159138663	11819046	0.0743	0.683

chr8	146364022	11819771	0.0808	0.5164
chr9	141213431	5619595	0.0398	0.3418
chr10	135534747	9596726	0.0708	0.6624
chr11	135006516	5636291	0.0417	0.3842
chr12	133851895	6849181	0.0512	0.2807
chr13	115169878	3520379	0.0306	0.2103
chr14	107349540	3642065	0.0339	0.2577
chr15	102531392	3859320	0.0376	0.2367
chr16	90354753	5667989	0.0627	0.3351
chr17	81195210	4757681	0.0586	0.3389
chr18	78077248	5497186	0.0704	0.5122
chr19	59128983	4789791	0.081	0.6815
chr20	63025520	5079752	0.0806	0.383
chr21	48129895	3065749	0.0637	0.404
chr22	51304566	3020917	0.0589	0.3226
chrMT	16571	121936	7.3584	5.5724
chrX	155270560	11811541	0.0761	0.3665
chrY	59373566	617934	0.0104	0.3774

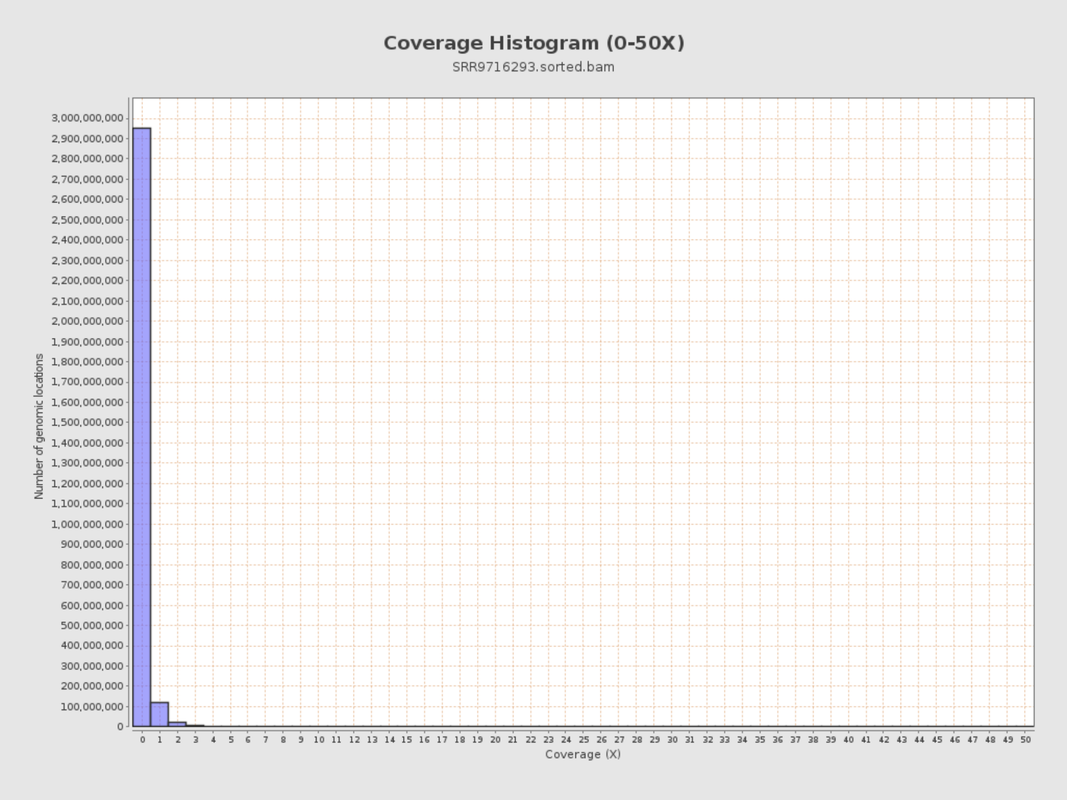
3. Results : Coverage across reference



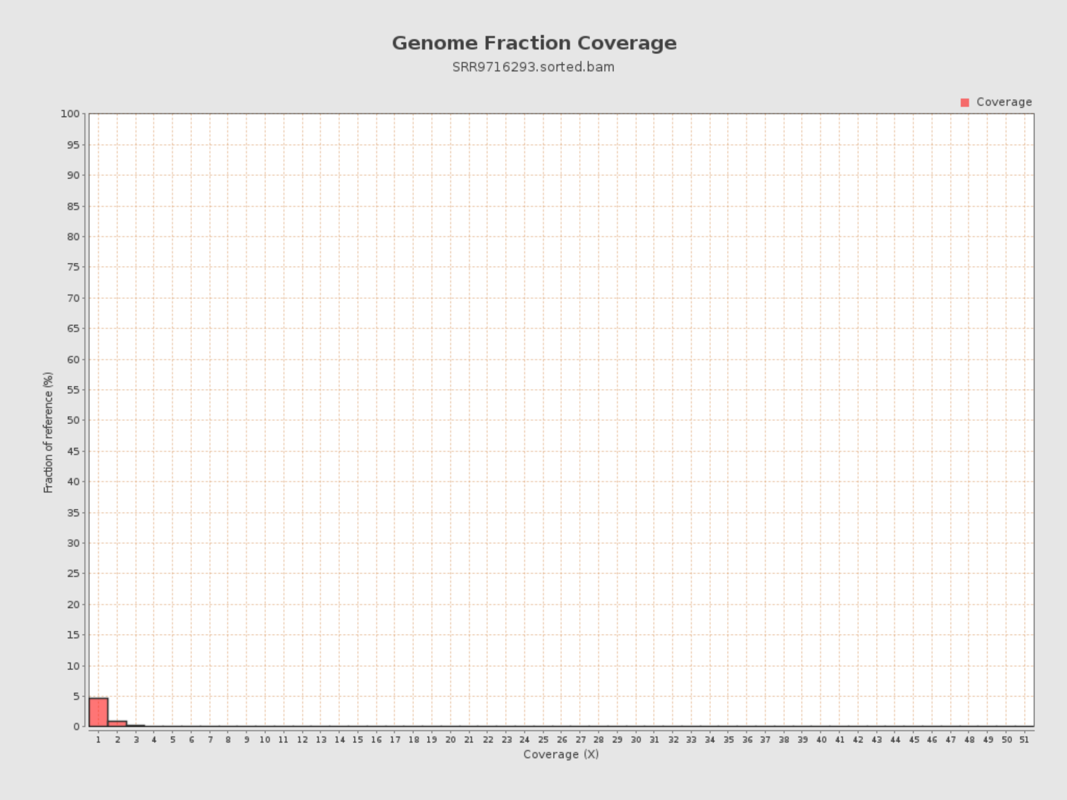
4. Results : Coverage Histogram



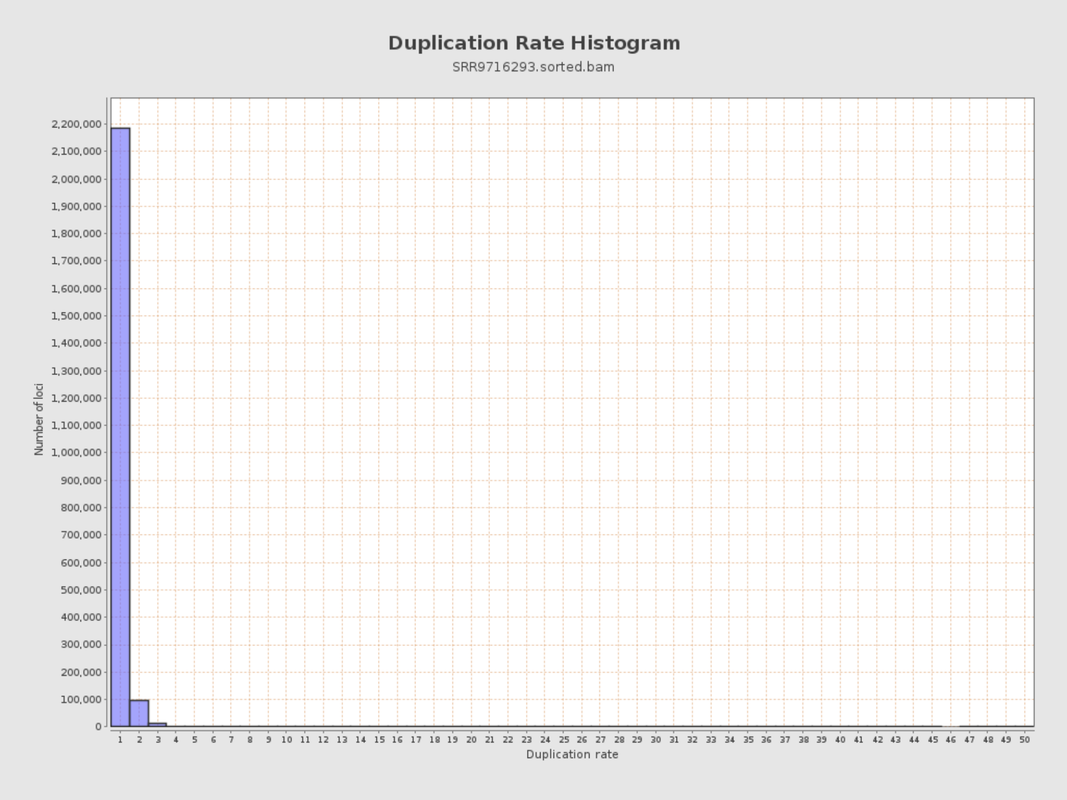
5. Results : Coverage Histogram (0-50X)



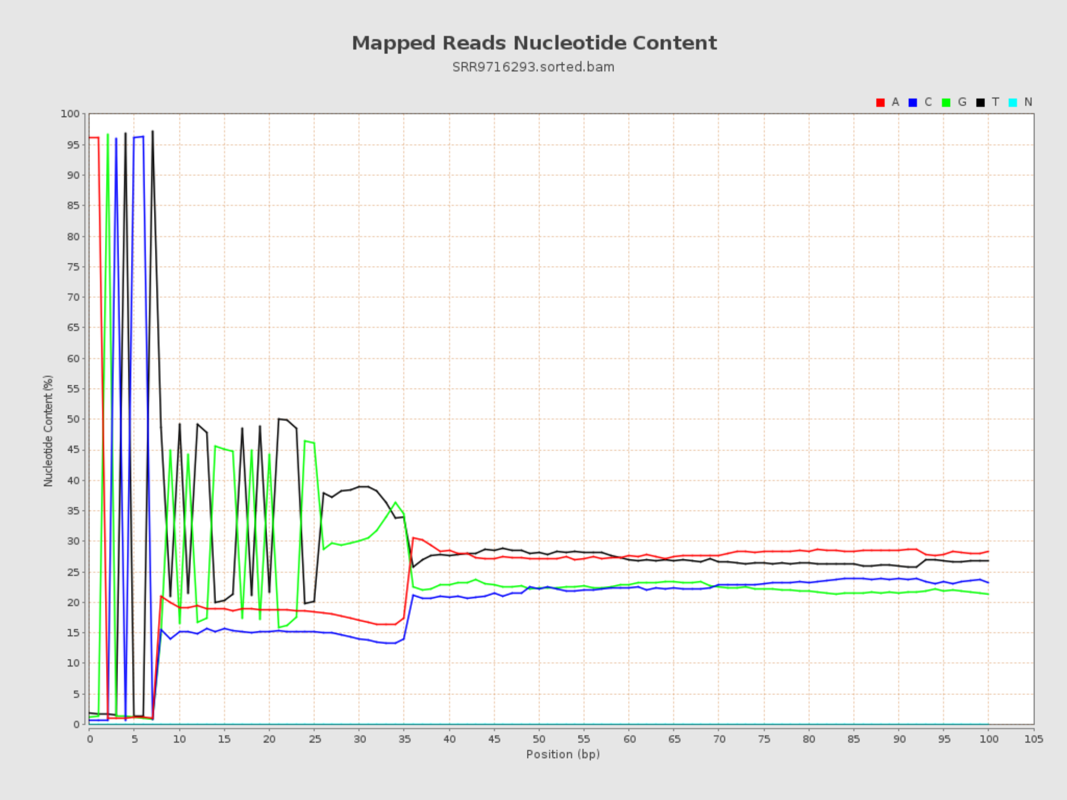
6. Results : Genome Fraction Coverage



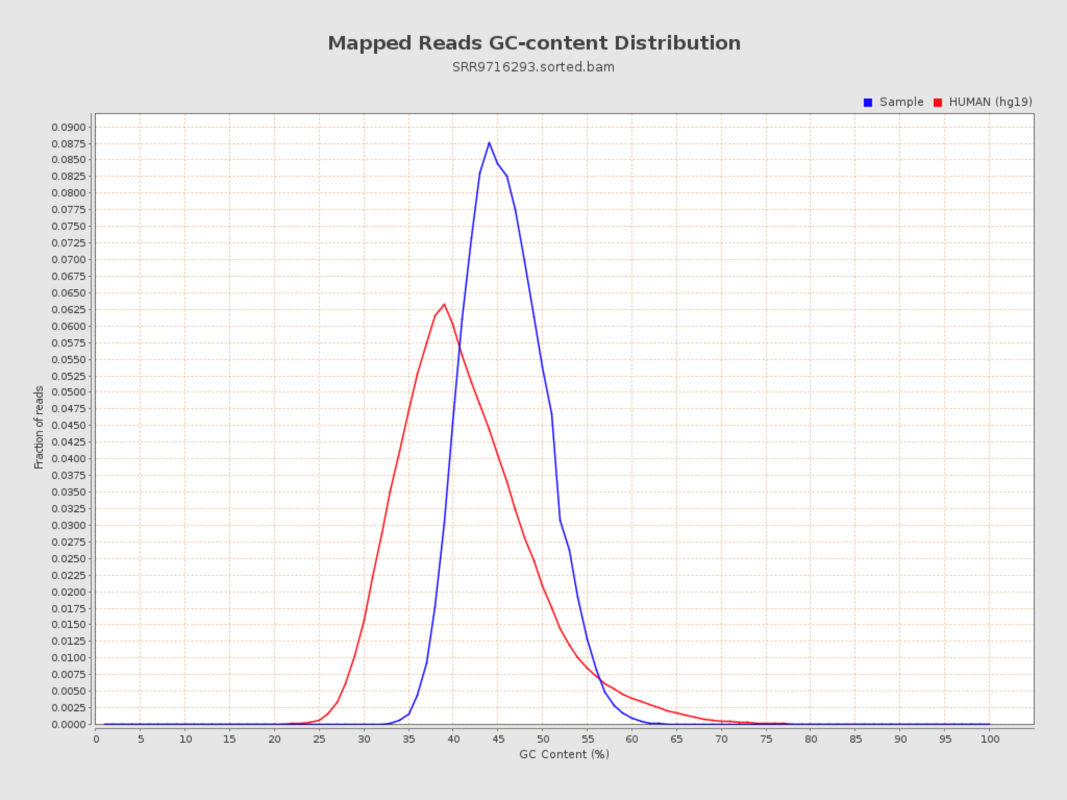
7. Results : Duplication Rate Histogram



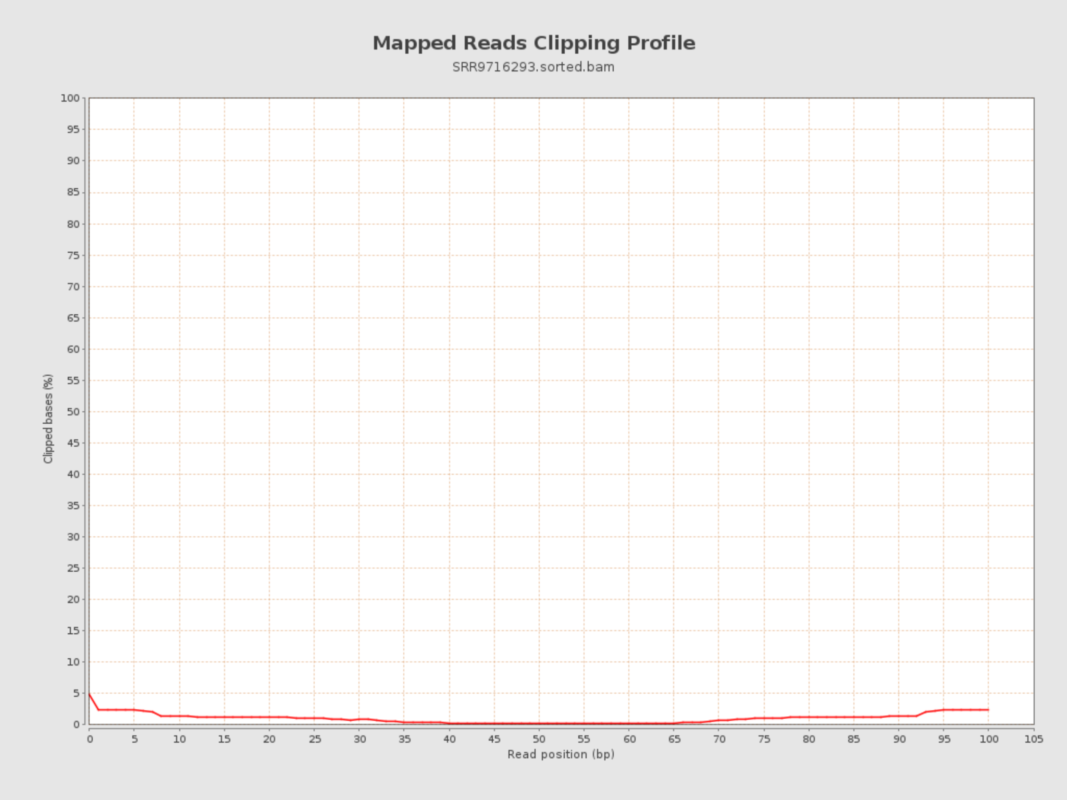
8. Results : Mapped Reads Nucleotide Content



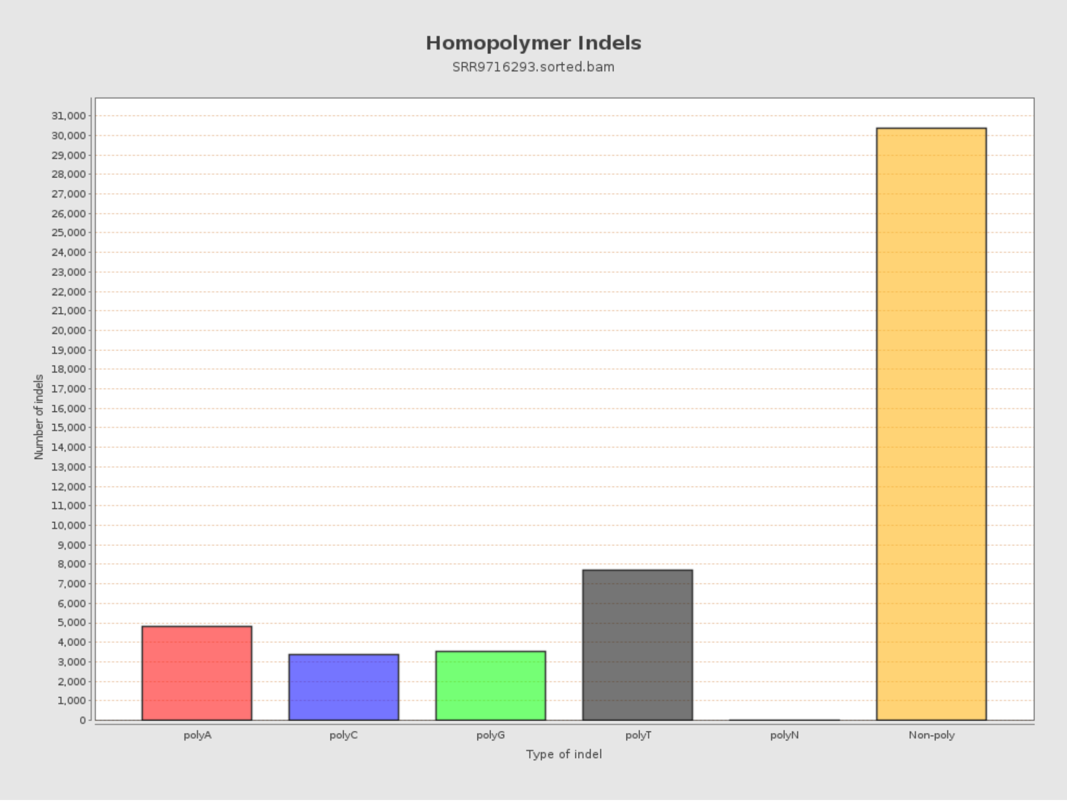
9. Results : Mapped Reads GC-content Distribution



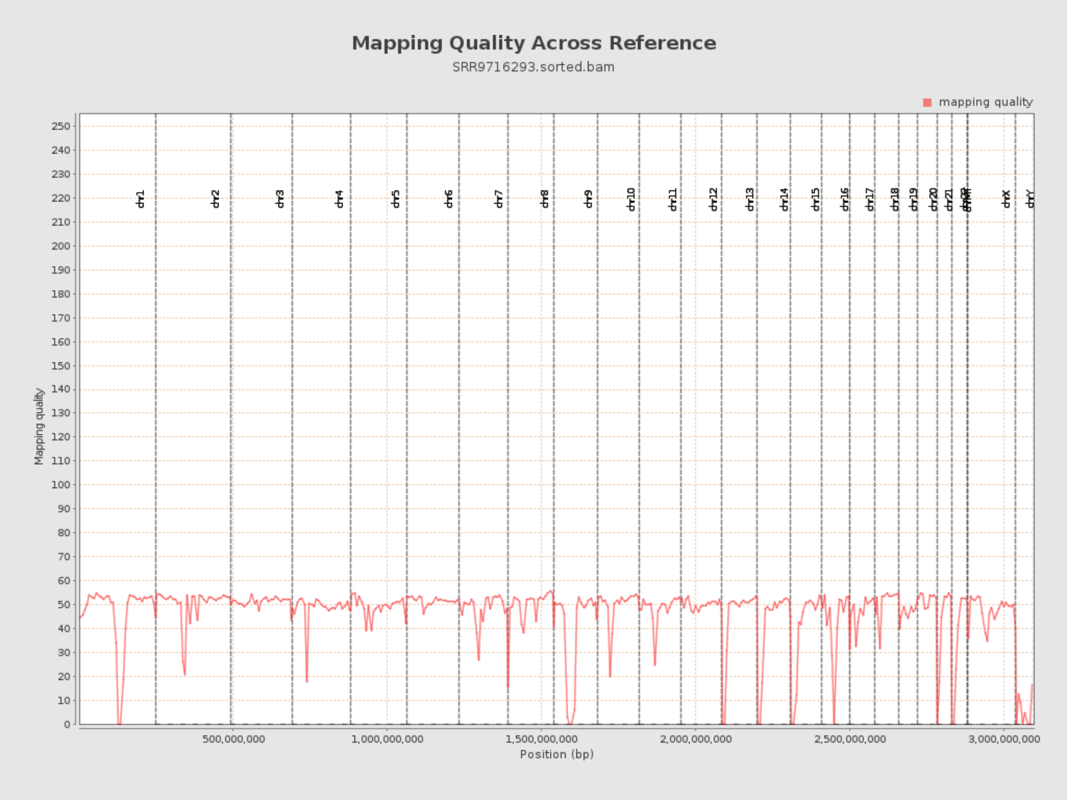
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram